

Maja Jagodic

List of Publications by Year in descending order

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Version: 2024-02-01

72
papers

6,895
citations

172207

29
h-index

91712

69
g-index

85
all docs

85
docs citations

85
times ranked

12563
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparison of EM-seq and PBAT methylome library methods for low-input DNA. <i>Epigenetics</i> , 2022, 17, 1195-1204.	1.3	19
2	DNA methylation changes in glial cells of the normal-appearing white matter in Multiple Sclerosis patients. <i>Epigenetics</i> , 2022, 17, 1311-1330.	1.3	10
3	Methylome and transcriptome signature of bronchoalveolar cells from multiple sclerosis patients in relation to smoking. <i>Multiple Sclerosis Journal</i> , 2021, 27, 1014-1026.	1.4	12
4	STATegra: Multi-Omics Data Integration – A Conceptual Scheme With a Bioinformatics Pipeline. <i>Frontiers in Genetics</i> , 2021, 12, 620453.	1.1	24
5	Small noncoding RNA profiling across cellular and biofluid compartments and their implications for multiple sclerosis immunopathology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	15
6	A validated generally applicable approach using the systematic assessment of disease modules by GWAS reveals a multi-omic module strongly associated with risk factors in multiple sclerosis. <i>BMC Genomics</i> , 2021, 22, 631.	1.2	5
7	Deep characterization of paired chromatin and transcriptomes in four immune cell types from multiple sclerosis patients. <i>Epigenomics</i> , 2021, 13, 1607-1618.	1.0	4
8	Longitudinal DNA methylation changes at MET may alter HGF/c-MET signalling in adolescents at risk for depression. <i>Epigenetics</i> , 2020, 15, 646-663.	1.3	12
9	Microglial autophagy-associated phagocytosis is essential for recovery from neuroinflammation. <i>Science Immunology</i> , 2020, 5, .	5.6	89
10	GeneSetCluster: a tool for summarizing and integrating gene-set analysis results. <i>BMC Bioinformatics</i> , 2020, 21, 443.	1.2	13
11	Gsta4 controls apoptosis of differentiating adult oligodendrocytes during homeostasis and remyelination via the mitochondria-associated Fas-Casp8-Bid-axis. <i>Nature Communications</i> , 2020, 11, 4071.	5.8	31
12	Effect of Vitamin D on Experimental Autoimmune Neuroinflammation Is Dependent on Haplotypes Comprising Naturally Occurring Allelic Variants of CIITA (Mhc2ta). <i>Frontiers in Neurology</i> , 2020, 11, 600401.	1.1	6
13	Epigenetic insights into multiple sclerosis disease progression. <i>Journal of Internal Medicine</i> , 2020, 288, 82-102.	2.7	21
14	C-type lectin receptors Mcl and Mincl control development of multiple sclerosis-like neuroinflammation. <i>Journal of Clinical Investigation</i> , 2020, 130, 838-852.	3.9	27
15	Non-parametric combination analysis of multiple data types enables detection of novel regulatory mechanisms in T cells of multiple sclerosis patients. <i>Scientific Reports</i> , 2019, 9, 11996.	1.6	13
16	Therapeutic efficacy of dimethyl fumarate in relapsing-remitting multiple sclerosis associates with ROS pathway in monocytes. <i>Nature Communications</i> , 2019, 10, 3081.	5.8	97
17	Tobacco smoking induces changes in true DNA methylation, hydroxymethylation and gene expression in bronchoalveolar lavage cells. <i>EBioMedicine</i> , 2019, 46, 290-304.	2.7	48
18	IL-22 Binding Protein Promotes the Disease Process in Multiple Sclerosis. <i>Journal of Immunology</i> , 2019, 203, 888-898.	0.4	13

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19	Different epigenetic clocks reflect distinct pathophysiological features of multiple sclerosis. <i>Epigenomics</i> , 2019, 11, 1429-1439.	1.0	22
20	Multiple sclerosis genomic map implicates peripheral immune cells and microglia in susceptibility. <i>Science</i> , 2019, 365, .	6.0	710
21	Neuronal methylome reveals CREB-associated neuro-axonal impairment in multiple sclerosis. <i>Clinical Epigenetics</i> , 2019, 11, 86.	1.8	24
22	Small non-coding RNAs as important players, biomarkers and therapeutic targets in multiple sclerosis: A comprehensive overview. <i>Journal of Autoimmunity</i> , 2019, 101, 17-25.	3.0	58
23	Combining evidence from four immune cell types identifies DNA methylation patterns that implicate functionally distinct pathways during Multiple Sclerosis progression. <i>EBioMedicine</i> , 2019, 43, 411-423.	2.7	45
24	Human skin long noncoding RNA WAKMAR1 regulates wound healing by enhancing keratinocyte migration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 9443-9452.	3.3	48
25	miR-31 regulates energy metabolism and is suppressed in T cells from patients with Sjögren's syndrome. <i>European Journal of Immunology</i> , 2019, 49, 313-322.	1.6	10
26	DNA Methylation in Multiple Sclerosis. <i>RNA Technologies</i> , 2019, , 181-214.	0.2	0
27	Genome-Wide Screen for MicroRNAs Reveals a Role for miR-203 in Melanoma Metastasis. <i>Journal of Investigative Dermatology</i> , 2018, 138, 882-892.	0.3	34
28	Fatal demyelinating disease is induced by monocyte-derived macrophages in the absence of TGF- β 2 signaling. <i>Nature Immunology</i> , 2018, 19, 1-7.	7.0	62
29	Local Delivery of miR-21 Stabilizes Fibrous Caps in Vulnerable Atherosclerotic Lesions. <i>Molecular Therapy</i> , 2018, 26, 1040-1055.	3.7	75
30	Impact of genetic risk loci for multiple sclerosis on expression of proximal genes in patients. <i>Human Molecular Genetics</i> , 2018, 27, 912-928.	1.4	41
31	Changes in methylation within the STK32B promoter are associated with an increased risk for generalized anxiety disorder in adolescents. <i>Journal of Psychiatric Research</i> , 2018, 102, 44-51.	1.5	16
32	Hypermethylation of <i>MIR21</i> in CD4+ T cells from patients with relapsing-remitting multiple sclerosis associates with lower miRNA-21 levels and concomitant up-regulation of its target genes. <i>Multiple Sclerosis Journal</i> , 2018, 24, 1288-1300.	1.4	33
33	Competitive repopulation of an empty microglial niche yields functionally distinct subsets of microglia-like cells. <i>Nature Communications</i> , 2018, 9, 4845.	5.8	148
34	Identification of MS-specific serum miRNAs in an international multicenter study. <i>Neurology: Neuroimmunology and NeuroInflammation</i> , 2018, 5, e491.	3.1	59
35	DNA methylation as a mediator of HLA-DRB1*15:01 and a protective variant in multiple sclerosis. <i>Nature Communications</i> , 2018, 9, 2397.	5.8	147
36	VAV1 regulates experimental autoimmune arthritis and is associated with anti-CCP negative rheumatoid arthritis. <i>Genes and Immunity</i> , 2017, 18, 48-56.	2.2	15

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37	Functional genomics analysis of vitamin D effects on CD4+ T cells in vivo in experimental autoimmune encephalomyelitis. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1678-E1687.	3.3	81
38	DNA methylation mediates genotype and smoking interaction in the development of anti-citrullinated peptide antibody-positive rheumatoid arthritis. Arthritis Research and Therapy, 2017, 19, 71.	1.6	48
39	Epigenetic research in multiple sclerosis: progress, challenges, and opportunities. Physiological Genomics, 2017, 49, 447-461.	1.0	30
40	Smoking induces DNA methylation changes in Multiple Sclerosis patients with exposure-response relationship. Scientific Reports, 2017, 7, 14589.	1.6	55
41	<sc>IL</sc>-22 binding protein regulates murine skin inflammation. Experimental Dermatology, 2017, 26, 444-446.	1.4	7
42	Epigenetics and multiple sclerosis. , 2017, , 185-213.		2
43	Usability of human Infinium MethylationEPIC BeadChip for mouse DNA methylation studies. BMC Bioinformatics, 2017, 18, 486.	1.2	25
44	Circulating miR-150 in CSF is a novel candidate biomarker for multiple sclerosis. Neurology: Neuroimmunology and NeuroInflammation, 2016, 3, e219.	3.1	92
45	BAFF-secreting neutrophils drive plasma cell responses during emergency granulopoiesis. Journal of Experimental Medicine, 2016, 213, 1537-1553.	4.2	66
46	Rat bone marrow-derived dendritic cells generated with GM-CSF/IL-4 or FLT3L exhibit distinct phenotypical and functional characteristics. Journal of Leukocyte Biology, 2016, 99, 437-446.	1.5	18
47	MOG-induced experimental autoimmune encephalomyelitis in the rat species triggers anti-neurofascin antibody response that is genetically regulated. Journal of Neuroinflammation, 2015, 12, 194.	3.1	8
48	Translational utility of experimental autoimmune encephalomyelitis: recent developments. Journal of Inflammation Research, 2015, 8, 211.	1.6	4
49	Genomic imprinting: A missing piece of the Multiple Sclerosis puzzle?. International Journal of Biochemistry and Cell Biology, 2015, 67, 49-57.	1.2	21
50	MicroRNAs as promising novel biomarkers and potential drug targets for inflammatory neurological diseases. Journal of the Neurological Sciences, 2015, 356, 3-4.	0.3	3
51	The multiple sclerosis risk gene IL22RA2 contributes to a more severe murine autoimmune neuroinflammation. Genes and Immunity, 2014, 15, 457-465.	2.2	39
52	Parent-of-Origin Effects Implicate Epigenetic Regulation of Experimental Autoimmune Encephalomyelitis and Identify Imprinted Dlk1 as a Novel Risk Gene. PLoS Genetics, 2014, 10, e1004265.	1.5	16
53	Natural Polymorphisms in Tap2 Influence Negative Selection and CD4 ^{hi} CD8 Lineage Commitment in the Rat. PLoS Genetics, 2014, 10, e1004151.	1.5	16
54	Acute treatment with valproic acid and l-thyroxine ameliorates clinical signs of experimental autoimmune encephalomyelitis and prevents brain pathology in DA rats. Neurobiology of Disease, 2014, 71, 220-233.	2.1	34

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55	Positional Gene Cloning in Experimental Populations. <i>Methods in Molecular Biology</i> , 2014, 1304, 3-24.	0.4	0
56	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. <i>Nature Genetics</i> , 2013, 45, 1353-1360.	9.4	1,213
57	Efficacy of vitamin D in treating multiple sclerosis-like neuroinflammation depends on developmental stage. <i>Experimental Neurology</i> , 2013, 249, 39-48.	2.0	66
58	Combined sequence-based and genetic mapping analysis of complex traits in outbred rats. <i>Nature Genetics</i> , 2013, 45, 767-775.	9.4	176
59	Combining genetic mapping with genome-wide expression in experimental autoimmune encephalomyelitis highlights a gene network enriched for T cell functions and candidate genes regulating autoimmunity. <i>Human Molecular Genetics</i> , 2013, 22, 4952-4966.	1.4	11
60	Next-Generation Sequencing Identifies MicroRNAs that Associate with Pathogenic Autoimmune Neuroinflammation in Rats. <i>Journal of Immunology</i> , 2013, 190, 4066-4075.	0.4	44
61	An evaluation of analysis pipelines for DNA methylation profiling using the Illumina HumanMethylation450 BeadChip platform. <i>Epigenetics</i> , 2013, 8, 333-346.	1.3	192
62	Anti-MOG antibodies are under polygenic regulation with the most significant control coming from the C-type lectin-like gene locus. <i>Genes and Immunity</i> , 2013, 14, 409-419.	2.2	11
63	Nurture your scientific curiosity early in your research career. <i>Nature Genetics</i> , 2013, 45, 116-118.	9.4	0
64	A Silent Exonic SNP in Kdm3a Affects Nucleic Acids Structure but Does Not Regulate Experimental Autoimmune Encephalomyelitis. <i>PLoS ONE</i> , 2013, 8, e81912.	1.1	1
65	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. <i>Nature</i> , 2011, 476, 214-219.	13.7	2,400
66	Multiple loci comprising immune-related genes regulate experimental neuroinflammation. <i>Genes and Immunity</i> , 2010, 11, 21-36.	2.2	20
67	A Role for <i>VAV1</i> in Experimental Autoimmune Encephalomyelitis and Multiple Sclerosis. <i>Science Translational Medicine</i> , 2009, 1, 10ra21.	5.8	52
68	Characterization of Multiple Sclerosis candidate gene expression kinetics in rat experimental autoimmune encephalomyelitis. <i>Journal of Neuroimmunology</i> , 2009, 210, 30-39.	1.1	22
69	Combined-cross analysis of genome-wide linkage scans for experimental autoimmune encephalomyelitis in rat. <i>Genomics</i> , 2006, 88, 737-744.	1.3	10
70	Resolution of a 16.8-Mb Autoimmunity-Regulating Rat Chromosome 4 Region into Multiple Encephalomyelitis Quantitative Trait Loci and Evidence for Epistasis. <i>Journal of Immunology</i> , 2005, 174, 918-924.	0.4	24
71	An Advanced Intercross Line Resolves <i>Eae18</i> into Two Narrow Quantitative Trait Loci Syntenic to Multiple Sclerosis Candidate Loci. <i>Journal of Immunology</i> , 2004, 173, 1366-1373.	0.4	44
72	Congenic mapping confirms a locus on rat chromosome 10 conferring strong protection against myelin oligodendrocyte glycoprotein-induced experimental autoimmune encephalomyelitis. <i>Immunogenetics</i> , 2001, 53, 410-415.	1.2	29